

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE GENERAL HOSPITAL CORPORATION  
FRUIT STREET  
BOSTON, MA 02114  
UNITED STATES OF AMERICA

APPLICANT/INVENTOR: de la Monte, Suzanne  
Wands, Jack R.

(ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
(B) STREET: 1100 New York Ave., Suite 600  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/038,908  
(B) FILING DATE: 26-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W.  
(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 0609.437PC01

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600  
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

0096467-092801

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC	50
Met Glu Phe Ser Leu Leu Pro Arg Leu Glu Cys	
1 5 10	
AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC	98
Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser	
15 20 25	
GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC	146
Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys	
30 35 40	
ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT	194
Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe	
45 50 55 60	
CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC	242
Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro	
65 70 75	
TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC	290
Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala	
80 85 90	
CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG	338
Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met	
95 100 105	
TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC	386
Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu	
110 115 120	
CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT	434
Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile	
125 130 135 140	
TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG	482
Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val	
145 150 155	
CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG	530
Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys	

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160	165	170	
CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His 175 180 185			578
CAC TAC ACC TGG CTA ATT TTT ATT TTT AAT TTT TTG AGA CAG His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln 190 195 200			626
AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly 205 210 215 220			674
TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser 225 230 235			722
CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CCG CTA GCT AAT TTT Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe 240 245 250			770
TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile 255 260 265			818
TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala 270 275 280			866
GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys 285 290 295 300			914
TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 305 310 315			962
CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe 320 325 330			1010
TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro 335 340 345			1058
CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr 350 355 360			1106
TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 365 370 375			1159
TCCTAAAGTGC TGGGATTACA GGCCTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA			1219

109200 8 2 21 9 6 6 6

AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGSTCTCAA CTCTGCGCTT	1279
CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTA AACAGTTACA	1339
TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	1399
GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA	1442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Phe	Ser	Leu	Leu	Leu	Pro	Arg	Leu	Glu	Cys	Asn	Gly	Ala	Ile	
1				5					10					15		
Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser	Asp	Ser	Pro	Ala	
			20					25					30			
Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys	Thr	His	Ala	Arg	
		35					40					45				
Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe	Leu	His	Val	Gly	
	50					55					60					
Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro	Ser	Val	Ser	Ala	
	65				70					75					80	
Ser	Gln	Ser	Ala	Arg	Tyr	Arg	Thr	Gly	His	His	Ala	Arg	Leu	Cys	Leu	
			85						90					95		
Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	Cys	Pro	Ser	Trp	
			100				105						110			
Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	Pro	Lys	Cys	Trp	
	115						120						125			
Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	Leu	Phe	Phe	Leu	
	130					135					140					
Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	Gln	Trp	Cys	Asp	
	145				150				155					160		
His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	His	Pro	Pro	Ala	
			165						170				175			
Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	His	Tyr	Thr	Trp	
			180					185					190			

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Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser  
195 200 205

Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro  
210 215

Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser  
225 230 235 240

Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu  
245 250 255

Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly  
260 265 270

Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly  
275 280 285

Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met  
290 295 300

Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly  
305 310 315 320

Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser  
325 330 335

Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn  
340 345 350

Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp  
355 360 365

Ser Gln Thr Pro Asp Leu Arg  
370 375

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTT GAGATGGAGT TTTGCTCTT GTTGCCGAGG CTGGAGTGCA ATGGCGCAAT	60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120
AGTAGCTGGG ATTACAGGCA TGTGACCAC GCTCGGCTAA TTTTGTATTT TTTTITAGTA	180

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GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC	240
TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC	300
TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTCTACTGA TGTGCCCCAA GCTGGTCTCC	360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGCTCAGCC	420
GTGCCTGGCC TTTTATTTT ATTTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT	480
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC	540
TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGSTAATT	600
TTTATTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC	660
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCTCCCGG GTTCAAGTTA TTCTCTGCC	720
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTGTAT	780
TTTGTAGATA GATGGGGTTT CACCATGTTC GCCAGGTTGA TCTTGATCTC TTGACCTTGT	840
GATCTGCTG CCTCGGCTA CCCAAAGTGC TGGGATTACA GGTCTGACT CCACGCCGGC	900
CTATTTTAA TTTTGTGTTT TTTGAAATGG AATCTCACTC TGTACCCAG GTCGGAGTGC	960
AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGG TCAAGCGATT CTCCTGTCTC	1020
AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT	1080
CATTAGAGGC GGGTTTACCA TATTTGTGAG GCTGGGTCTC AAATCTCTGA CCTCAGGTGA	1140
CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC	1200
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC	1260
TCAAACCTCT GCCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT	1320
TTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA	1380
C	1381

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1418 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCGAGG CTGGAGTGCA ATGGCGCAAT	60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120
AGTAGGCTGG GATTACAGCG ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTAGT	180
AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT	240
CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCG GCCTCTGCCT	300
GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGTCGT CTCCTGAGCT	360
CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGCGTG CAGCGTGCC	420
TGGCCTTTTT ATTTATTTT TTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT	480
GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC	540
TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTAT	600
TTTTATTTT AATTTTGTG GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTCAGTG	660
GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CTGCCCCAG	720
CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTT TTGTATTTT	780
AGTAGAGATG GGGTTTCACC ATGTTGCGCA GGTGATGTG AGATCTCTTG ACCTGTGTAT	840
CTGCCTGCCT CGGCCTCCCA AAGTGTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC	900
TATTTTAAAT TTTTGTGTT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA	960
ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT	1020
CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCGCTAA TTTTGTATT	1080
TTATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAATCC TGACCTCAGG	1140
TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGGGTGAGC CTCACCCAGC	1200
CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG	1260
GTCTCAAAT TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACCCC AGCCAGTCAC	1320
ATTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG	1380
AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT	1418

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

09964578.092801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

22

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

24

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

09064678.092801

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

00064678-002801

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: de la Monte, Suzanne  
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
  - (B) STREET: 1100 New York Ave., Suite 600
  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Esmond, Robert W.
  - (B) REGISTRATION NUMBER: 32,893
  - (C) REFERENCE/DOCKET NUMBER: 0609.4370000
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 202-371-2600
  - (B) TELEFAX: 202-371-2540

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1442 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 15..1139
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC  
 Met Glu Phe Ser Leu Leu Pro Arg Leu Glu Cys  
 1 5 10

AAT Asn	GGC Gly	GCA Ala	ATC Ile	TCA Ser	GCT Ala	CAC His	CGC Arg	AAC Asn	CTC Leu	CGC Arg	CTC Leu	CCG Pro	GGT Gly	TCA Ser	AGC Ser	98
	15						20					25				
GAT Asp	TCT Ser	CCT Pro	GCC Ala	TCA Ser	GCC Ala	TCC Ser	CCA Pro	GTA Val	GCT Ala	GGG Gly	ATT Ile	ACA Thr	GGC Gly	ATG Met	TGC Cys	146
	30					35					40					
ACC Thr	CAC His	GCT Ala	CGG Arg	CTA Leu	ATT Ile	TTG Leu	TAT Tyr	TTT Phe	TTT Phe	TTA Leu	GTA Val	GAG Glu	ATG Met	GAG Glu	TTT Phe	194
	45				50					55					60	
CTC Leu	CAT His	GTT Val	GGT Gly	CAG Gln	GCT Ala	GGT Gly	CTC Leu	GAA Glu	CTC Leu	CCG Pro	ACC Thr	TCA Ser	GAT Asp	GAT Asp	CCC Pro	242
				65					70					75		
TCC Ser	GTC Val	TCG Ser	GCC Ala	TCC Ser	CAA Gln	AGT Ser	GCT Ala	AGA Arg	TAC Tyr	AGG Arg	ACT Thr	GGC Gly	CAC His	CAT His	GCC Ala	290
			80					85					90			
CGG Arg	CTC Leu	TGC Cys	CTG Leu	GCT Ala	AAT Asn	TTT Phe	TGT Cys	GGT Gly	AGA Arg	AAC Asn	AGG Arg	GTT Val	TCA Ser	CTG Leu	ATG Met	338
		95					100					105				
TGC Cys	CCA Pro	AGC Ser	TGG Trp	TCT Ser	CCT Pro	GAG Glu	CTC Leu	AAG Lys	CAG Gln	TCC Ser	ACC Thr	TGC Cys	CTC Leu	AGC Ser	CTC Leu	386
	110				115						120					
CCA Pro	AAG Lys	TGC Cys	TGG Trp	GAT Asp	TAC Tyr	AGG Arg	CGT Arg	GCA Ala	GCC Ala	GTG Val	CCT Pro	GGC Gly	CTT Leu	TTT Phe	ATT Ile	434
	125				130					135					140	
TTA Leu	TTT Phe	TTT Phe	TTA Leu	AGA Arg	CAC His	AGG Arg	TGT Cys	CCC Pro	ACT Thr	CTT Leu	ACC Thr	CAG Gln	GAT Asp	GAA Glu	GTG Val	482
				145					150					155		
CAG Gln	TGG Trp	TGT Cys	GAT Asp	CAC His	AGC Ser	TCA Ser	CTG Leu	CAG Gln	CCT Pro	TCA Ser	ACT Thr	CCT Pro	GAG Glu	ATC Ile	AAG Lys	530
			160					165					170			
CAT His	CCT Pro	CCT Pro	GCC Ala	TCA Ser	GCC Ala	TCC Ser	CAA Gln	GTA Val	GCT Ala	GGG Gly	ACC Thr	AAA Lys	GAC Asp	ATG Met	CAC His	578
		175					180					185				
CAC His	TAC Tyr	ACC Thr	TGG Trp	CTA Leu	ATT Ile	TTT Phe	ATT Ile	TTT Phe	ATT Ile	TTT Phe	AAT Asn	TTT Phe	TTG Leu	AGA Arg	CAG Gln	626
	190				195						200					
AGT Ser	CTC Leu	AAC Asn	TCT Ser	GTC Val	ACC Thr	CAG Gln	GCT Ala	GGA Gly	GTG Val	CAG Gln	TGG Trp	CGC Arg	AAT Asn	CTT Leu	GGC Gly	674
	205				210				215					220		
TCA Ser	CTG Leu	CAA Gln	CCT Pro	CTG Pro	CCT Pro	CCC Gly	GGG Phe	TTC Lys	AAG Phe	TTA Leu	TTC Phe	TCC Ser	TGC Cys	CCC Pro	AGC Ser	722
			225					230						235		
CTC Leu	CTG Leu	AGT Ser	AGC Trp	TGG Asp	GAC Tyr	TAC Arg	AGG Arg	CGC Pro	CCA Pro	CCA Pro	CGC Arg	CTA Leu	GCT Ala	AAT Asn	TTT Phe	770
			240					245					250			
TTT Phe	GTA Val	TTT Phe	TTA Leu	GTA Val	GAG Glu	ATG Met	GGG Gly	TTC Phe	ACC Thr	ATG Met	TTC Phe	GCC Ala	AGG Arg	TTG Leu	ATC Ile	818
	255						260					265				
TTG ATC	ATC TCT	TCT GGA	CCT TGT	GAT CTG	CTG CCT	GCC TCG	CGC GCC	TCC CAA	AGT GCT							866

Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala	
270 275 280	
GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT	914
Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys	
285 290 295 300	
TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG	962
Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp	
305 310 315	
CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC	1010
Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe	
320 325 330	
TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA	1058
Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro	
335 340 345	
CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT	1106
His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr	
350 355 360	
TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT	1159
Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg	
365 370 375	
TCCAAAGTGC TGGGATTACA GGCCTGAGCC ACCTCACCCA GCCGCGTAAT TTAGATAAAA	1219
AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCCT	1279
CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTA AACAGTTACA	1339
TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	1399
GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA	1442

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile	
1 5 10 15	
Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala	
20 25 30	
Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg	
35 40 45	
Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly	
50 55 60	
Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala	
65 70 75 80	
Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu	

Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp  
 100 105 110

Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp  
 115 120 125

Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu  
 130 135 140

Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp  
 145 150 155 160

His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala  
 165 170 175

Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp  
 180 185 190

Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser  
 195 200 205

Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro  
 210 215 220

Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser  
 225 230 235 240

Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu  
 245 250 255

Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly  
 260 265 270

Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly  
 275 280 285

Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met  
 290 295 300

Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly  
 305 310 315 320

Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser  
 325 330 335

Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn  
 340 345 350

Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp  
 355 360 365

Ser Gln Thr Pro Asp Leu Arg  
 370 375

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1381 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

09064678-092601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTT GAGATGGAGT TTTGCTCTTT GTTGCCCAAG CTGGAGTGCA ATGGCGCAAT 60  
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCTGCGCT CAGCCTCCCC 120  
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTITAGTA 180  
GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240  
TCCCCGCTCG GCCTGCCCAA AGTGTCTGAG TTACAGGCAT GAGCCACCAT GCCCGGCTCT 300  
TGCTTGGCTA ATTTTGTGG TAGAAACAGG GTTTCAGTGA TGTGCCCCAA GCTGGTCTCC 360  
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGCTCAGCC 420  
GTGCTTGGCC TTTTATTTTT ATTTTITTTA AGACACAGGT GTACCACTCT TACCCAGGAT 480  
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540  
TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CTTGGTAATT 600  
TTTATTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTACCCAGG GCTGGAGTGC 660  
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCTCCCGG GTTCAAGTTA TTCTCTTGCC 720  
CCAGCTCCTT GAGTAGCTGG GACTACAGGC GCCCACCAGC CCTAGCTAAT TTTTITGTAT 780  
TTTTAGTAGA GATGGGGTTT CACCATGTTT GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840  
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTGCTGACT CCACGCCGGC 900  
CTATTTTAA TTTTITGTTT TTTGAAATGG AATCTCACTC TGTATCCAGG GTCGGAGTGC 960  
AATGGCAAAT CTCGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC 1020  
AGCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT 1080  
CATTAGAGGC GGGTTTACCA TATTGTTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140  
CCCACCTGCC TCAGCTTCC AAAGTGTGG GATTACAGGC GTGAGCCACC TCACCAGCC 1200  
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260  
TCAAACCTCT GCCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320  
TTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380  
C 1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

09964678.092801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCGAG CTGGAGTGCA ATGGCGCAAT 60  
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120  
AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTTAT TTTTTTAGT 180  
AGAGATGGAG TTTCCTCATG TTGGTCAGGC TGGTCTCGAA CTCGACCTC AGATGATCCT 240  
CCCCTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCG GCCTCTGCCT 300  
GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGTGGT CTCTTGAGCT 360  
CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGCGGTG CAGCCGTGCC 420  
TGGCCTTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480  
GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540  
TCAGCCTCCC AAAGTAGCTG GGACCAAGA CATGCACCAC TACACCTGGC TAATTTTAT 600  
TTTTTATTTT AATTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660  
GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CTTGCCCCAG 720  
CCTCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGTATTTTT 780  
AGTAGAGATG GGGTTTCACC ATGTTCCGCA GGTGTGATGT AGATCTCTTG ACCTTGTGAT 840  
CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC 900  
TATTTTTTAA TTTTGTTTGT TTGAAATGGA ATCTCACTCT GTTACCACAG CTGGAGTGCA 960  
ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCTGTCT 1020  
CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCGCGTAA TTTTGTATT 1080  
TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAACCTC TGACCTCAGG 1140  
TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GCGTGCAGC CTCACCCAGC 1200  
CGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG 1260  
GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC 1320  
ATTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG 1380  
AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT 1418

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

0964578-092801



TGTCCTCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCA

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

00054578.002301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

0954578.092801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

09964678.092801